Amendments to the Specification

Please replace the paragraph on page 11, line 11, with the following amended paragraph:

FIG. 10 is a Mondrian of BAC AL049839~~-A049839~~.

Please replace the paragraph on page 21, line 29 through page 22, line 6 with the following amended paragraph:

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH or REPEATMASKER, the latter available on-line at the RepeatMasker website developed by Smit & Green, ~~http://ftp.genome.washington.edu/RM/RepeatMasker.html,~~ or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Please replace the paragraph on page 33, lines 21 - 33 with the following amended paragraph:

For amplification, the putative exons selected in process 300 are input into one or more primer design programs, such as PRIMER3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Krawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology.* Humana Press, Totowa, NJ, pp 365-386) ~~(available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/)~~, with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about exons predicted to be no

more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for exons predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Please replace the paragraph on page 36, lines 17 - 26 with the following amended paragraph:

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, available online at the Pat Brown Laboratory website at Stanford University ~~http://cmgm.stanford.edu/pbrown/mguide/index.html~~), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

Please replace the paragraph on page 65, line 23 through page 66, line 2 with the following amended paragraph:

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function. For example, addition of a fourth gene prediction program, such as GENSCAN (GENSCAN web server at the Burge Laboratory at MIT; also see: Burge and Karlin, *J. Mol. Biol.* 268, 78-94 (1997) and Burge, C. B. Modeling dependencies in pre-mRNA splicing signals. In Salzberg, S., Searls, D. and Kasif, S., eds. Computational Methods in Molecular Biology, Elsevier Science, Amsterdam, pp. 127-163 (1998).) ~~(http://genes.mit.edu/GENSCANinfo.html)~~,

to the three gene prediction programs used in our first experiments (GRAIL, GENEFINDER, DICTION) would be accommodated by a fourth series of rectangles disposed horizontally in field 81, but offset vertically from rectangles 81a, 81b, and 81c.

Please replace the paragraph on page 74, lines 14 - 28 with the following amended paragraph:

Accordingly, after selecting the largest exon per gene bin, a 500 bp fragment of sequence centered on the exon was passed to the primer picking software, PRIMER3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Krawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology.* Humana Press, Totowa, NJ, pp 365-386) ~~(available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/)~~. A first additional sequence was commonly added to each exon-unique 5' primer, and a second, different, additional sequence was commonly added to each exon-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some exons be found to warrant further study.